Amendments to the Specification

Please replace the paragraph beginning at page 19, line 13, with the amended numbered paragraph below:

[0091] Protein sequencing of the 40 kDa band yielded both amino terminal sequences and some internal sequences generated by protease digestion (Table 1--SEQ ID NOS: 1-4). Insufficient yields of the 60 kDa band resulted in unreliable sequence information. Unfortunately, efforts to amplify PCR products utilizing redundant primers designed to these sequences were not successful. In mid 2000, an EST (#BE005912) was entered into the GCG database, which contained homology to the 40 kDa band sequence as shown in Table 1 (SEQ ID NOS: 5 and 6). The translation of this EST indicated good homology to the amino terminal sequence of the 40 kDa repeat (e.g. ~~PGSRKFKTTE~~ residues 2-12 of SEQ ID NO:6) with only one amino acid difference (i.e. an asparagine is present instead of phenylalanine in the EST sequence). Also, some of the internal sequences are partially conserved (e.g. SEQ ID NO: 2 and to a lesser extent, SEQ ID NO: 3 and SEQ ID NO: 4). More importantly, all the internal sequences are preceded by a basic amino acid (Table 1, indicated by arrows) appropriate for proteolysis by the trypsin used to create the internal peptides from the 40 kDa cyanogen bromide repeat. Utilizing the combined sequences, those obtained by amino acid sequencing and those identified in the EST (#BE005912) and a second EST (#AA640762) identified in the database, sense primers were created as follows: 5'-GGA GAG GGT TCT GCA GGG TC-3' (SEQ ID NO: 7) representing amino acids ERVLQG and anti-sense primer, 5' GTG AAT GGT ATC AGG AGA GG-3' (SEQ ID NO: 9) representing PLLIPF. Using PCR, the presence of transcripts was confirmed representing these sequences in ovarian tumors and their absence in normal ovary and either very low levels or no detectable levels in a mucinous tumor (FIG. 2A). The existence of transcripts was further confirmed in cDNA derived from multiple primary ovarian carcinoma cell lines and the absence of transcripts in matched lymphocyte cultures from the same patient (FIG. 2B).